



SEQUENCE LISTING

GENERAL INFORMATION

- (i) APPLICANT: McCarthy, Sean
- (ii) TITLE OF INVENTION: NOVEL CRSP-1 COMPOSITIONS AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 - (B) STREET: One Post Office Square
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-2170
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/842,898
 - (B) FILING DATE: 17-APR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Arnold, Beth E.
 - (B) REGISTRATION NUMBER: 35,430
 - (C) REFERENCE/DOCKET NUMBER: MAA-004.02
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-832-1000
 - (B) TELEFAX: 617-832-7000

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 38..1087

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGG GCGGGCGGCT GCGGGCGCAG AGCGGAG ATG CAG CGG CTT GGG GCC	55
Met Gln Arg Leu Gly Ala	
1 5	
ACC CTG CTG TGC CTG CTG CTG GCG GCG GCG GTC CCC ACG GCC CCC GCG	103
Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala	
10 15 20	
CCC GCT CCG ACG GCG ACC TCG GCT CCA GTC AAG CCC GGC CCG GCT CTC	151
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu	
25 30 35	
AGC TAC CCG CAG GAG GAG GCC ACC CTC AAT GAG ATG TTC CGC GAG GTT	199
Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val	
40 45 50	
GAG GAA CTG ATG GAG GAC ACG CAG CAC AAA TTG CGC AGC GCG GTG GAA	247
Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu	
55 60 65 70	
GAG ATG GAG GCA GAA GAA GCT GCT GCT AAA GCA TCA TCA GAA GTG AAC	295
Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn	
75 80 85	
CTG GCA AAC TTA CCT CCC AGC TAT CAC AAT GAG ACC AAC ACA GAC ACG	343
Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr	
90 95 100	
AAC GTT GGA AAT AAT ACC ATC CAT GTG CAC CGA GAA ATT CAC AAG ATA	391
Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile	
105 110 115	
ACC AAC AAC CAG ACT GGA CAA ATG GTC TTT TCA GAG ACA GTT ATC ACA	439
Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr	
120 125 130	
TCT GTG GGA GAC GAA GAA GGC AGA AGG AGC CAC GAG TGC ATC ATC GAC	487
Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp	
135 140 145 150	
GAG GAC TGT GGG CCC AGC ATG TAC TGC CAG TTT GCC AGC TTC CAG TAC	535
Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr	
155 160 165	
ACC TGC CAG CCA TGC CGG GGC CAG AGG ATG CTC TGC ACC CGG GAC AGT	583
Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser	
170 175 180	
GAG TGC TGT GGA GAC CAG CTG TGT GTC TGG GGT CAC TGC ACC AAA ATG	631
Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met	
185 190 195	
GCC ACC AGG GGC AGC AAT GGG ACC ATC TGT GAC AAC CAG AGG GAC TGC	679
Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys	
200 205 210	
CAG CCG GGG CTG TGC TGT GCC TTC CAG AGA GGC CTG CTG TTC CCT GTG	727
Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val	
215 220 225 230	

TGC ACA CCC CTG CCC GTG GAG GGC GAG CTT TGC CAT GAC CCC GCC AGC	775
Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser	
235 240 245	
CGG CTT CTG GAC CTC ATC ACC TGG GAG CTA GAG CCT GAT GGA GCC TTG	823
Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu	
250 255 260	
GAC CGA TGC CCT TGT GCC AGT GGC CTC CTC TGC CAG CCC CAC AGC CAC	871
Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His	
265 270 275	
AGC CTG GTG TAT GTG TGC AAG CCG ACC TTC GTG GGG AGC CGT GAC CAA	919
Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln	
280 285 290	
GAT GGG GAG ATC CTG CTG CCC AGA GAG GTC CCC GAT GAG TAT GAA GTT	967
Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val	
295 300 305 310	
GGC AGC TTC ATG GAG GAG GTG CGC CAG GAG CTG GAG GAC CTG GAG AGG	1015
Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg	
315 320 325	
AGC CTG ACT GAA GAG ATG GCG CTG AGG GAG CCT GCG GCT GCC GCC GCT	1063
Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala Ala	
330 335 340	
GCA CTG CTG GGA AGG GAA GAG ATT TAGATCTGGA CCAGGCTGTG GGTAGATGTG	1117
Ala Leu Leu Gly Arg Glu Glu Ile	
345 350	
CAATAGAAAT AGCTAATTTA TTTCCCCANG TGTGTGCTTT AAGCGTGGGC TG	1169

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala	
1 5 10 15	
Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val	
20 25 30	
Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn	
35 40 45	
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys	
50 55 60	
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys	
65 70 75 80	

Ala	Ser	Ser	Glu	Val	Asn	Leu	Ala	Asn	Leu	Pro	Pro	Ser	Tyr	His	Asn	
				85					90						95	
Glu	Thr	Asn	Thr	Asp	Thr	Asn	Val	Gly	Asn	Asn	Thr	Ile	His	Val	His	
			100					105					110			
Arg	Glu	Ile	His	Lys	Ile	Thr	Asn	Asn	Gln	Thr	Gly	Gln	Met	Val	Phe	
		115					120					125				
Ser	Glu	Thr	Val	Ile	Thr	Ser	Val	Gly	Asp	Glu	Glu	Gly	Arg	Arg	Ser	
	130					135					140					
His	Glu	Cys	Ile	Ile	Asp	Glu	Asp	Cys	Gly	Pro	Ser	Met	Tyr	Cys	Gln	
145					150					155					160	
Phe	Ala	Ser	Phe	Gln	Tyr	Thr	Cys	Gln	Pro	Cys	Arg	Gly	Gln	Arg	Met	
			165						170					175		
Leu	Cys	Thr	Arg	Asp	Ser	Glu	Cys	Cys	Gly	Asp	Gln	Leu	Cys	Val	Trp	
			180					185					190			
Gly	His	Cys	Thr	Lys	Met	Ala	Thr	Arg	Gly	Ser	Asn	Gly	Thr	Ile	Cys	
	195					200						205				
Asp	Asn	Gln	Arg	Asp	Cys	Gln	Pro	Gly	Leu	Cys	Cys	Ala	Phe	Gln	Arg	
	210					215					220					
Gly	Leu	Leu	Phe	Pro	Val	Cys	Thr	Pro	Leu	Pro	Val	Glu	Gly	Glu	Leu	
225					230				235						240	
Cys	His	Asp	Pro	Ala	Ser	Arg	Leu	Leu	Asp	Leu	Ile	Thr	Trp	Glu	Leu	
			245					250					255			
Glu	Pro	Asp	Gly	Ala	Leu	Asp	Arg	Cys	Pro	Cys	Ala	Ser	Gly	Leu	Leu	
		260					265						270			
Cys	Gln	Pro	His	Ser	His	Ser	Leu	Val	Tyr	Val	Cys	Lys	Pro	Thr	Phe	
	275						280					285				
Val	Gly	Ser	Arg	Asp	Gln	Asp	Gly	Glu	Ile	Leu	Leu	Pro	Arg	Glu	Val	
	290				295						300					
Pro	Asp	Glu	Tyr	Glu	Val	Gly	Ser	Phe	Met	Glu	Glu	Val	Arg	Gln	Glu	
305					310					315					320	
Leu	Glu	Asp	Leu	Glu	Arg	Ser	Leu	Thr	Glu	Glu	Met	Ala	Leu	Arg	Glu	
			325					330					335			
Pro	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Gly	Arg	Glu	Glu	Ile			
		340					345						350			

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ATGCAGCGGC TTGGGGCCAC CCTGCTGTGC CTGCTGCTGG CGGCGGCGGT CCCACGGCC      60
CCCGCGCCCG CTCCGACGGC GACCTCGGCT CCAGTCAAGC CCGGCCCGGC TCTCAGCTAC      120
CCGCAGGAGG AGGCCACCCT CAATGAGATG TTCCGCGAGG TTGAGGAACT GATGGAGGAC      180
ACGCAGCACA AATTGCGCAG CGCGGTGGAA GAGATGGAGG CAGAAGAAGC TGCTGCTAAA      240
GCATCATCAG AAGTGAACCT GGCAAACCTA CCTCCCAGCT ATCACAATGA GACCAACACA      300
GACACGAACG TTGGAAATAA TACCATCCAT GTGCACCGAG AAATTCACAA GATAACCAAC      360
AACCAGACTG GACAAATGGT CTTTTCAGAG ACAGTTATCA CATCTGTGGG AGACGAAGAA      420
GGCAGAAGGA GCCACGAGTG CATCATCGAC GAGGACTGTG GGCCCAGCAT GTACTGCCAG      480
TTTGCCAGCT TCCAGTACAC CTGCCAGCCA TGCCGGGGGCC AGAGGATGCT CTGCACCCGG      540
GACAGTGAGT GCTGTGGAGA CCAGCTGTGT GTCTGGGGTC ACTGCACCAA AATGGCCACC      600
AGGGGCAGCA ATGGGACCAT CTGTGACAAC CAGAGGGACT GCCAGCCGGG GCTGTGCTGT      660
GCCTTCCAGA GAGGCCTGCT GTTCCCTGTG TGCACACCCC TGCCCGTGGA GGGCGAGCTT      720
TGCCATGACC CCGCCAGCCG GCTTCTGGAC CTCATCACCT GGGAGCTAGA GCCTGATGGA      780
GCCTTGGACC GATGCCCTTG TGCCAGTGGC CTCTCTGCC AGCCCCACAG CCACAGCCTG      840
GTGTATGTGT GCAAGCCGAC CTTCGTGGGG AGCCGTGACC AAGATGGGGA GATCCTGCTG      900
CCCAGAGAGG TCCCCGATGA GTATGAAGTT GGCAGCTTCA TGGAGGAGGT GCGCCAGGAG      960
CTGGAGGACC TGGAGAGGAG CCTGACTGAA GAGATGGCGC TGAGGGAGCC TGCGGCTGCC      1020
GCCGCTGCAC TGCTGGGAAG GGAAGAGATT                                     1050

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Arg Arg Gly Glu Gly Pro Ala Pro Arg Arg Arg Trp Leu Leu Leu
1           5           10           15

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Leu Ala Val Leu Ala Ala Leu Cys Cys Ala Ala Ala Gly Ser Gly Gly
20           25           30

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Arg Arg Arg Ala Ala Ser Leu Gly Glu Met Leu Arg Glu Val Glu Ala
 35 40 45
 Leu Met Glu Asp Thr Gln His Lys Leu Arg Asn Ala Val Gln Glu Met
 50 55 60
 Glu Ala Glu Glu Glu Gly Ala Lys Lys Leu Ser Glu Val Asn Phe Glu
 65 70 75 80
 Asn Leu Pro Pro Thr Tyr His Asn Glu Ser Asn Thr Glu Thr Arg Ile
 85 90 95
 Gly Asn Lys Thr Val Gln Thr His Gln Glu Ile Asp Lys Val Thr Asp
 100 105 110
 Asn Arg Thr Gly Ser Thr Ile Phe Ser Glu Thr Ile Ile Thr Ser Ile
 115 120 125
 Lys Gly Gly Glu Asn Lys Arg Asn His Glu Cys Ile Ile Asp Glu Asp
 130 135 140
 Cys Glu Thr Gly Lys Tyr Cys Gln Phe Ser Thr Phe Glu Tyr Lys Cys
 145 150 155 160
 Gln Pro Cys Lys Thr Gln His Thr His Cys Ser Arg Asp Val Glu Cys
 165 170 175
 Cys Gly Asp Gln Leu Cys Val Trp Gly Glu Cys Arg Lys Ala Thr Ser
 180 185 190
 Arg Gly Glu Asn Gly Thr Ile Cys Glu Asn Gln His Asp Cys Asn Pro
 195 200 205
 Gly Thr Cys Cys Ala Phe Gln Lys Glu Leu Leu Phe Pro Val Cys Thr
 210 215 220
 Pro Leu Pro Glu Glu Gly Glu Pro Cys His Asp Pro Ser Asn Arg Leu
 225 230 235 240
 Leu Asn Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Val Leu Glu Arg
 245 250 255
 Cys Pro Cys Ala Ser Gly Leu Ile Cys Gln Pro Gln Ser Ser His Ser
 260 265 270
 Thr Thr Ser Val Cys Glu Leu Ser Ser Asn Glu Thr Arg Lys Asn Glu
 275 280 285
 Lys Glu Asp Pro Leu Asn Met Asp Glu Met Pro Phe Ile Ser Leu Ile
 290 295 300
 Pro Arg Asp Ile Leu Ser Asp Tyr Glu Glu Ser Ser Val Ile Gln Glu
 305 310 315 320
 Val Arg Lys Glu Leu Glu Ser Leu Glu Asp Gln Ala Gly Val Lys Ser
 325 330 335
 Glu His Asp Pro Ala His Asp Leu Phe Leu Gly Asp Glu Ile
 340 345 350